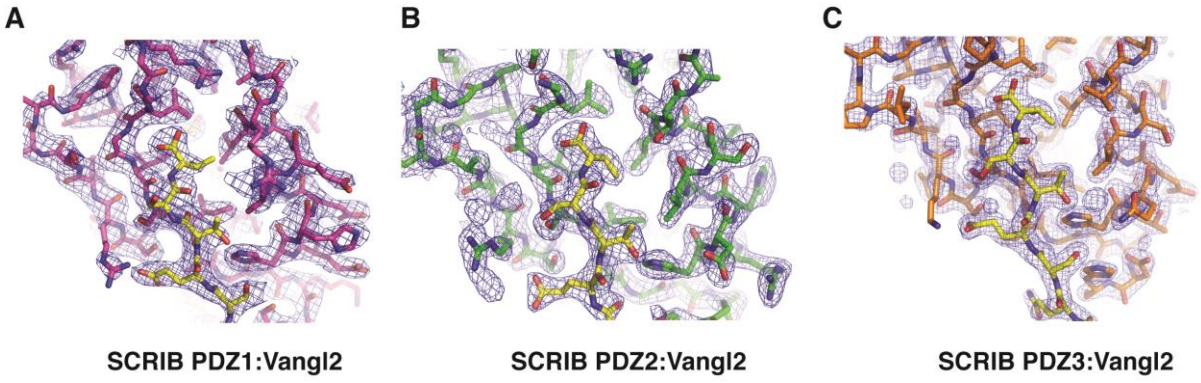
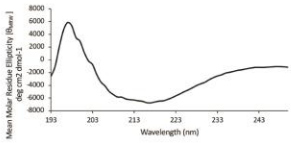
Expanded view figure legends

FIGURE EV2: 2Fo-Fc electron density maps of PDZ1, PDZ2 and PDZ3 complexes with Vangl2 as well as PDZ2 on its own. A) Electron density map encompassing the binding groove of Scribble PDZ1 (magenta sticks) in complex with Vangl2 peptide (yellow sticks). The electron density map is shown as a blue mesh contoured at 1.5 σ. **B)** Electron density map encompassing the binding groove of Scribble PDZ2 (green sticks) in complex with Vangl2 (yellow sticks). The electron density map is shown as a blue mesh contoured at 1.5 σ. **C)** Electron density map encompassing the binding groove of Scribble PDZ3 (orange sticks) in complex with Vangl2 peptide (yellow sticks). The electron density map is shown as a blue mesh contoured at 1.5 σ.

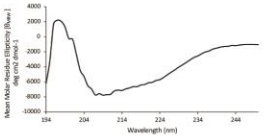
FIGURE EV3: Circular dichroism spectroscopy of wild type and mutant Scribble PDZ1, PDZ2, PDZ3 and PDZ4 domains.

Circular dichroism spectra recorded for wild type and mutant Scribble PDZ1,2,3 and 4 domains indicated that there were no major spectral differences between the proteins, suggesting that they were similarly folded, with mutations not leading to unfolding of the PDZ domains.

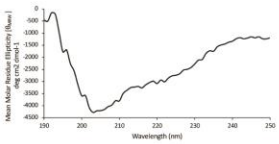

A
B
C
SCRIB PDZ1:Vangl2
SCRIB PDZ2:Vangl2
SCRIB PDZ3:Vangl2



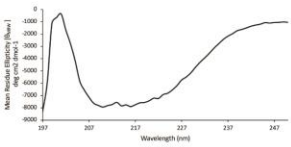
PDZ1 WT



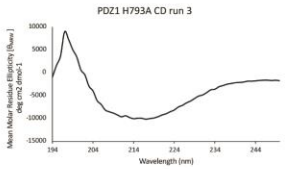
PDZ2 WT



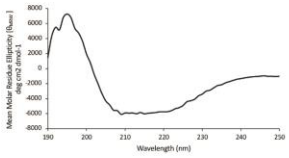
PDZ3 WT



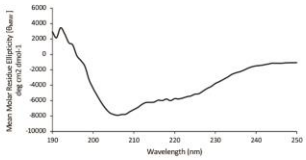
PDZ4 WT



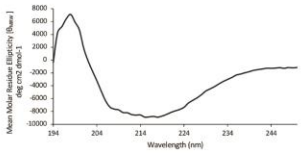
PDZ1 H793A



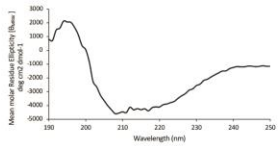
PDZ2 R896A



PDZ3 P1043L



PDZ1 Q808H



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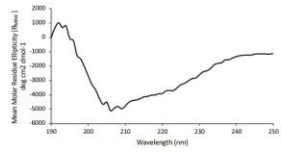

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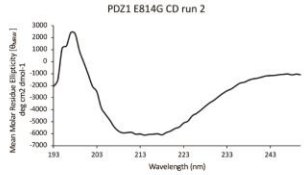

PDZ1 E814G

Table EV1: X-ray crystallographic data collection and refinement statistics.

	PDZ1:Vangl2	PDZ2 apo	PDZ2:Vangl2	PDZ3:Vangl2
Data collection				
Space group	C 1 2 1	P 1	I $2_12_12_1$	P 4_12_12
No of molecules in AU	4+4	4	4+4	2+2
Cell dimensions				
a, *b*, *c* (Å)	219.37, 53.09, 53.52	37.89, 41.69, 49.02	78.05, 60.77, 96.02	54.71, 54.71, 129.98
α, β, γ (°)	90.00, 104.12, 90.00	90.27, 91.96, 105.84	90.00, 106.48, 90.00	90.00, 90.00, 90.00
Wavelength (Å)	0.9537	0.9537	0.9537	0.9537
Resolution (Å)*	51.51-2.20 (2.28-2.20)	31.60-2.44 (2.53-2.44)	47.17-2.50 (2.59-2.50)	37.08-1.95 (2.02-1.95)
R_{sym} or R_{merge}*	0.066 (0.620)	0.121 0.650)	0.076 (0.425)	0.060 (0.763)
$I / \sigma I$*	8.3 (1.6)	10.5 (2.1)	16.2 (4.5)	38.4 (5.5)
CC(1/2)	0.999 (0.743)	0.994 (0.792)	0.999 (0.856)	1.000 (0.952)
Completeness (%)*	99.9 (100.0)	98.3 98.0)	91.5 (93.2)	99.9 (99.93)
Redundancy*	5.0 (5.1)	3.9 (3.9)	5.7 (5.7)	27.6 (28.6)
Wilson B-factor	49.57	28.24	30.84	34.1
Refinement				
Resolution (Å)	51.51-2.20	31.60-2.44	47.17-2.50	37.08-1.95
No. reflections	30485	10507	13813	15101
R_{work} / R_{free}	0.260/0.288	0.225/0.269	0.236/0.270	0.223/0.262
No. non-hydrogen atoms				
Protein	3238	2699	2777	1328
Ligand/ion	111	8	32	-
Water	46	81	98	81
B-factors				
Protein	68.66	32.90	35.60	46.36
Ligand/ion	71.34	37.21	42.39	-
Water	59.55	31.71	31.62	45.70
R.m.s. deviations				
Bond lengths (Å)	0.006	0.004	0.003	0.004
Bond angle (°)	1.09	1.01	0.68	1.03
Ramachandran plot (%)				
Favored	97.8	97.4	98.1	99.4
Allowed	2.2	2.6	1.9	0.6
Disallowed	0	0	0	0